AMENDMENTS

In the Claims:

Please add the following claims 184-219:

184. The method according to claim 118 wherein the selected samples comprise antibodies that form an antigen-antibody complex with an amino acid sequence of less than about 100 contiguous amino acids encoded by a hepatitis C virus genome.

185. The method according to claim 119 wherein the selected samples comprise antibodies that form an antigen-antibody complex with an amino acid sequence of less than about 100 contiguous amino acids encoded by an HCV cDNA insert in the lambda gt-11 library deposited as ATCC deposit No. 40394.

186. The method according to claim 123 wherein the selected samples comprise antibodies that form an antigen-antibody complex with an amino acid sequence of less than about 100 contiguous amino acids found in Figure 90.

187. The method according to claim 124 wherein the selected samples comprise antibodies that form an antigen-antibody complex with an amino acid sequence of less than about 100 contiguous amino acids found in Figure 14.

188. The method according to claim 125 wherein the selected samples comprise antibodies that form an antigen-antibody complex with an amino acid sequence of less than about 100 contiguous amino acids encoded by an HCV cDNA insert in a lambda gt-11 library deposited as ATCC deposit No. 40394.

189. A method according to any one of claim 118, 119, 123-125, wherein the selected samples comprise one or more contiguous amino acid sequences selected from the following group:

AA1-AA50; AA1-AA84; AA9-AA177; AA1-AA120; AA35-AA45; AA50-AA100; AA40-AA90; AA65-AA75; AA80-AA90; AA99-AA120; AA95-AA110; AA100-AA150; AA150-AA200; AA200-AA250; AA220-AA240; AA245-AA265; AA250-AA300; AA290-

AA330; AA290-AA305; AA300-AA-350; AA310-AA330; AA350-AA400;AA405-AA495; AA400-AA450; AA437-AA582; AA450-AA500; AA475-AA495;AA500-AA550; AA511-AA690; AA515-AA550; AA550-AA600; AA550-AA625; AA575-AA605; AA600-AA650; AA600-AA625; AA635-AA665; AA650-AA700; AA645-AA680; AA700-AA750; AA700-AA725; AA725-AA775; AA770-AA790; AA750-AA800; AA800-AA815; AA850-AA875; AA800-AA850; AA920-AA990; AA850-AA900; AA920-AA945; AA940-AA965; AA950-AA1000; AA1000-AA1060; AA1000-AA1050; AA1025-AA1040; AA1075-AA1175-AA1000; AA1000-AA1060; AA1000-AA1050; AA1025-AA1040; AA1075-AA1175; AA1050-AA1200; AA1070-AA1100; AA1100-AA1140; AA1192-AA1457; AA1195-AA1250; AA1200-AA1225; AA1225-AA1250; AA1250-AA1300; AA1260-AA1310; AA1260-AA1280; AA1266-AA1428; AA1300-AA1350; AA1310-AA1340; AA1345-AA1405; AA1350-AA1400; AA1365-AA1380; AA1380-AA1405; AA1400-AA1450; AA1450-AA1500; AA1475-AA1515; AA1475-AA1500; AA1500-AA1550; AA1515-AA1550; AA1550-AA1600; AA1569-AA1931; AA1570-AA1590; AA1595-AA1610; AA1590-AA1650; AA1610-AA1645; AA1650-AA1690; AA1685-AA1770; AA1689-AA1805; AA1690-AA1720; AA1694-AA1735; AA1720-AA1745; AA1745-AA1770; AA1750-AA1800; AA1775-AA1810; AA1795-AA1850; AA1850-AA1900; AA1900-AA1950; AA1900-AA1920; AA1916-AA2021; AA1920-AA1940; AA1949-AA2124; AA1950-AA2000; AA1950-AA1985; AA2000-AA2050; AA2020-AA2045; AA2045-AA2100; AA2045-AA2070; AA2054-AA2223; AA2070-AA2100; AA2100-AA2150; AA2150-AA2220; AA2200-AA2345; AA2250-AA2330; AA2265-AA2280; AA2280-AA2290; AA2287-AA2385; AA2300-AA2350; AA2350-AA2400; AA2345-AA2415; AA2345-AA2375; AA2348-AA2464; AA2370-AA2410; AA2400-AA2450; AA2400-AA2425; AA2415-AA2450; AA2445-AA2500; AA2371-AA2502; AA2500-AA2550; AA2505-AA2540; AA2550-AA2600; AA2560-AA2580; AA2600-AA2650; AA2620-AA2650; AA2650-AA2700; AA2655-AA2670; AA2670-AA2700; AA2700-AA2750; AA2750-AA2800; AA2755-AA2780; AA2780-AA2830; AA2785-AA2810; AA2796-AA2886;

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AA2810-AA2825; AA2800-AA2850; AA2850-AA2900; AA2900-AA2950; AA2910-AA2930; and AA2925-AA2950;

wherein the contiguous amino acid sequence is depicted according to the formula AA_x-AA_y, x and y denoting amino acid numbers HCV-1 polyprotein or corresponding regions of other HCV isolates.

190. The method according to claim 189 wherein said antibodies are detectable in an ELISA or radioimmunoassay.

191. The method according to claim 190 wherein said ELISA or radioimmunoassay employs an antigen comprising said amino acid sequence made by recombinant expression.

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192. The method according to claim 190 wherein said biological samples are blood.

193. The method according to claim 191 wherein said biological samples are blood.

194. The method according to claim 190 wherein said biological samples are plasma.

195. The method according to claim 191 wherein said biological samples are plasma.

196. The method according to claim 190 wherein said biological samples are sera.

197. The method according to claim 191 wherein said biological samples are sera.

198. The method according to claim 192 wherein the selecting is to identify an HCV positive sample for removal from the supply.

199. The method according to claim 193 wherein the selecting is to identify an HCV positive sample for removal from the supply.

200. The method according to claim 194 wherein the selecting is to identify an HCV positive sample for removal from the supply.

201. The method according to claim 195 wherein the selecting is to identify an HCV positive sample for removal from the supply.

202. The method according to claim 196 wherein the selecting is to identify an HCV positive sample for removal from the supply.

203. The method according to claim 197 wherein the selecting is to identify an HCV positive sample for removal from the supply.

204. A method according to any one of claim 118, 119, 123-125, wherein the selected samples comprise one or more contiguous amino acid sequences selected from the following group:

AA1-AA84; AA437-AA582; AA511-AA690; AA9-AA177; AA1192-AA1457; AA1266-AA1428; AA1694-AA1735; AA1689-AA1805; AA1916-AA2021; AA1949-AA2124; AA2054-AA2223; AA2200-AA3325; AA2287-AA2385; AA2348-AA2464; AA2371-AA2502; AA2796-AA2886; AA1569-AA1931,

wherein the contiguous amino acid sequence is depicted according to the formula AA_x-AA_y, x and y denoting amino acid numbers HCV-1 polyprotein or corresponding regions of other HCV isolates.

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205. The method according to claim 204 wherein said antibodies are detectable in an ELISA or radioimmunoassay.

206. The method according to claim 205 wherein said ELISA or radioimmunoassay employs an antigen comprising said amino acid sequence made by recombinant expression.

207. The method according to claim 205 wherein said biological samples are blood.

208. The method according to claim 206 wherein said biological samples are blood.

209. The method according to claim 205 wherein said biological samples are plasma.

210. The method according to claim 206 wherein said biological samples are plasma.

211. The method according to claim 205 wherein said biological samples are sera.

212. The method according to claim 206 wherein said biological samples are sera.

213. The method according to claim 207 wherein the selecting is to identify an HCV positive sample for removal from the supply.

214. The method according to claim 208 wherein the selecting is to identify an HCV positive sample for removal from the supply.

215. The method according to claim 209 wherein the selecting is to identify an HCV positive sample for removal from the supply.

216. The method according to claim 210 wherein the selecting is to identify an HCV positive sample for removal from the supply.

217. The method according to claim 211 wherein the selecting is to identify an HCV positive sample for removal from the supply.

218. The method according to claim 212 wherein the selecting is to identify an HCV positive sample for removal from the supply.

219. A method according to any one of claim 118, 119, 123-125, wherein the selected samples comprise one or more contiguous amino acid sequences selected from the following group:

AA1694-AA1735; AA1569-AA1931; AA1192-AA1457; AA1-AA84; and AA9-AA177, wherein the contiguous amino acid sequence is depicted according to the formula AA_x-AA_y, x and y denoting amino acid numbers of HCV-1 polyprotein or corresponding regions of other HCV isolates.

220. A method of selecting biological samples from a supply of biological samples comprising selecting from said supply those samples that contain a detectable polynucleotide comprising a contiguous sequence of at least 15 nucleotides from either strand of at least one of the hepatitis C virus (HCV) cDNA inserts in a lambda gt-11 cDNA library deposited as ATCC No. 40394.

221. The method according to claim 115, wherein the detectable polynucleotide comprises a contiguous sequence of less than about 90 nucleotides fully complementary to either strand of Figure 3.

222. The method according to claim 116, wherein the detectable polynucleotide comprises a contiguous sequence of less than about 90 nucleotides fully complementary to either strand of Figure 62A.

223. The method according to claim 117, wherein the detectable polynucleotide comprises a contiguous sequence of less than about 90 nucleotides fully complementary to either strand of Figure 89.

224. The method according to claim 118, wherein the selected samples comprise a polynucleotide that hybridizes under stringent conditions to a polynucleotide that comprises a contiguous sequence of less than about 90 nucleotides from the genome of a hepatitis C virus genome or the complement thereof.

225. The method according to claim 119, wherein the selected samples comprise a polynucleotide that hybridizes under stringent conditions to a contiguous sequence of less than about 90 nucleotides from either strand of at least one of the hepatitis C virus (HCV) cDNA inserts in a lambda gt-11 cDNA library deposited as ATCC No. 40394.

226. The method according to claim 120, wherein the selected samples comprise a polynucleotide that hybridizes under stringent conditions to a contiguous sequence of less than about 90 nucleotides fully complementary to either strand of Figure 89.

227. The method according to claim 121, wherein the selected samples comprise a polynucleotide that hybridizes under stringent conditions to a contiguous sequence of less than about 90 nucleotides fully complementary to either strand of Figure 14.

228. The method according to claim 115, wherein the detectable polynucleotide comprises a contiguous sequence of less than about 90 nucleotides from either strand of at least one of the hepatitis C virus (HCV) cDNA inserts in a lambda gt-11 cDNA library deposited as ATCC No. 40394.